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Glaxo Group Ltd  
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 35 40 45  
 Asp Gly Asn Trp Tyr Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly  
 50 55 60  
 Trp Lys Lys Ile Ala Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala  
 65 70 75 80  
 40 Met Lys Thr Gly Trp Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp  
 85 90 95  
 Ala Lys Glu Gly Ala Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp  
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 <213> *Streptococcus pneumoniae*

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 35 40 45

Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp Lys Trp Tyr Tyr  
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 65 70 75 80  
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 <213> *Streptococcus pneumoniae*

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 <212> DNA  
 <213> *Streptococcus pneumoniae*

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45  
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50  
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 <213> *Streptococcus pneumoniae*

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	gtaaaaataa 429	
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	aagtggact atttcaacga agaagggtcc atgaagacagc gctgggtcaa gtacaaggac 240	
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5 <210> 18  
 <211> 1947  
 <212> DNA  
 <213> Artificial Sequence

10 <220>  
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 epitope and human P501S.

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 <212> DNA  
 <213> Artificial Sequence

<220>  
 55 <223> Codon optimised human P501S

<400> 19

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 ccccttgcgtt cccttgcgtt gatgttggc gtttttttttgcgat cccggggatgc 180  
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<211> 1688
5 <212> DNA
<213> Artificial Sequence

<220>
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15 ggtgtctggc atttggggcc tcctggccct cgtgtgcgtg cctctcctcg gcagcgcttc 240
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40 cgaggcag 1688

<210> 22
<211> 1688
<212> DNA
45 <213> Artificial Sequence

<220>
<223> Codon optimised human P501S

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ggaggagggtc ctgttgcggcc ttttccatc gggggggccatc 660

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 cgtcgctgag ctctgttcctt ggtatggccct gatgacgttc 900  
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20 <210> 23  
 <211> 435  
 <212> DNA  
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25 <220>  
 <223> Hybrid gene between St. pneum. C-LytA, P2 T helper  
 epitope and a small portion of the 5' end of human  
 P501S

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 aatggcactt ggtactactt tgacaggatca ggctatatgc ttgcagaccc ctggaggaag 120  
 cacacagacg gcaactggta ctgggtcgac aactcaggcg 180  
 aaaatcgctg ataagtggta ctatccaac gaagaagggtg 240  
 35 aagtacaagg acacttggta ctacttagac gctaaagaag ggcgcattgca atacatcaag 300  
 gctactcta agttcattgg tatcaactgaa ggcgtatgg tatcaaatgc ctttatccag 360  
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40 <210> 24  
 <211> 435  
 <212> DNA  
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45 <220>  
 <223> Hybrid gene between St. pneum. C-LytA, P2 T helper  
 epitope and a small portion of the 5' end of human  
 P501S - codon-optimised

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 cacacgacg gcaactggta ctgggtcgat aactcggggag 180  
 aagatcgccg 240  
 55 aagtataagg acacctggta ctacctcgac gccaaggagg ggcgcattgca gtataatcaag 300  
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<212> DNA  
 <213> Artificial Sequence

5 <220>  
 <223> Hybrid gene between St. pneum. C-LytA, P2 T helper  
 epitope and a small portion of the 5' end of human  
 P501S - codon-optimised

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 cacaccgacg ggaactggta ctgggtcgac aactctggcg agatggctac ggggtggaag 180  
 aagatcgccg acaagtggta ctacttcaac gaggagggcg ccatgaagac cgggtgggtg 240  
 aagtacaagg acacctggta ctacctggac gctaaggagg ggcgcattgca gtacatcaag 300  
 15 gccaactcga agttcatcg gatcaccgag ggcgtatgg tcagtaacgc tttcatccag 360  
 agcgcggacg gcacaggctg gtattacctg aagcccgatg gcaccctggc ggacagac 420  
 gagaattca tgtac 435

20 <210> 26  
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 <212> DNA  
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25 <220>  
 <223> Hybrid gene between St. pneum. C-LytA, P2 T helper  
 epitope and a small portion of the 5' end of human  
 P501S - codon-optimised

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 ggccaccggc tggaaagaaga tcgcccacaa gtgtactat ttcaacgggg agggcccat 240  
 35 gaagaccggc tgggtgaagt ataaggacac ctgtactac ctcgacgcac aggagggcgc 300  
 catcgatcatcaaggcca acagaatgtt catcgatcc accgaggagg tggatggtcag 360  
 caacgcctt atccagagccg ccgacggcac cggatggta tacttgaagc cggacggcac 420  
 cctcgccgat cggcccgaga agttcatgtt ctgactcgag gcag 464

40 <210> 27  
 <211> 652  
 <212> PRT  
 <213> Artificial Sequence

45 <220>  
 <223> Hybrid protein between St. pneum. C-LytA, P2 T  
 helper epitope and amino acids 51-553 of human  
 P501S

50 <400> 27  
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 1 5 10 15  
 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Phe Asp Ser Ser Gly Tyr  
 20 25 30  
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp  
 35 40 45  
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp  
 50 55 60  
 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val  
 65 70 75 80  
 60 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met  
 85 90 95

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val  
 100 105 110  
 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr  
 115 120 125  
 5 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met  
 130 135 140  
 Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro  
 145 150 155 160  
 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg  
 10 165 170 175  
 Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe  
 180 185 190  
 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro  
 195 200 205  
 15 Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp  
 210 215 220  
 Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp  
 225 230 235 240  
 Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala  
 20 245 250 255  
 Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile  
 260 265 270  
 Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu  
 275 280 285  
 25 Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala  
 290 295 300  
 Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala  
 305 310 315 320  
 Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg  
 30 325 330 335  
 Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His  
 340 345 350  
 Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala  
 355 360 365  
 35 Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr  
 370 375 380  
 Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro  
 385 390 395 400  
 Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser  
 40 405 410 415  
 Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val  
 420 425 430  
 Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala  
 435 440 445  
 45 Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His  
 450 455 460  
 Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe  
 465 470 475 480  
 Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg  
 50 485 490 495  
 Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala  
 500 505 510  
 Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro  
 515 520 525  
 55 Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Ser Gly Leu  
 530 535 540  
 Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser  
 545 550 555 560  
 Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly  
 60 565 570 575  
 Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu

580	585	590	
Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser			
595	600	605	
Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val			
610	615	620	
Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala			
625	630	635	640
Lys Tyr Ser Ala Gly Gly His His His His His His His			
645	650		

10

<210> 28  
<211> 1959  
<212> DNA  
15 <213> Artificial Sequence

<220>  
<223> DNA encoding the Hybrid protein between St. pneum.  
C-LytA, P2 T helper epitope and amino acids 51-553  
20 of human P501S

<400> 28  
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aatggcatt ggtactactt tgacagttca ggctatatgc ttgcagacgg ctggaggaag 120  
25 cacacagacg gcaactggta ctgggtcgac aactcaggcg aaatggctac aggcttggaa 180  
aaaatcgctg aaataatggta ctatccaaac gagaagggtg ccatgaagac aggctgggtc 240  
aagtacaagg acacttggta ctacttagac gctaaagaag ggcgcattgca atacatcaag 300  
gctaaatcta agttcattgg tatcaactgaa gggttcatgg tatcaaatgc ctttatccag 360  
tcagcgacg gaacaggctg gtactaccc aaaccagacg gaacactggc agacaggcca 420  
30 gaaaagttca tgtacatggt gctgggcatt ggtccagtgc tgggcctgtt ctgtgtcccg 480  
ctcttaggtc cagccagtga ccactggcgt ggacgtatgc gccgcggccg gcccttcata 540  
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35 ctcttccggg accccggacca ctgtcgccag gcctactctg tctatgcctt catgtcagt 780  
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40 gaagggtctgt cggcccccctt cttgtcgccc cactgtgtc catgcgggc cccgttggct 1020  
ttccggaaacc tggggccctt gttccccgg ctgcaccaggc tttgtcgccg catgcggcc 1080  
accctcgccc ggctcttgcgtt ggctgagctg tgcagtgaa tggcactcat gacccatcg 1140  
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tgcctgtccc acagtgtggc cgtggtgaca gttcagccg ccctcaccgg gttcaccc 1440  
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ttccctggca aataccgagg ggacactgga ggtgtcttagca tggaggacag cctgtatgacc 1560  
50 agtttctgc caggccctaa gcctggagctt ccctccctta atggacacgt ggggtctggaa 1620  
ggcagtggcc tgcctccacc tccacccggc ctgtcgccggg cctctggctt tgatgtctcc 1680  
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atgggctcca ttgtccagctt cagccagtctt gtcactgcctt atatgtgtc tggccgcaggc 1860  
55 ctgggtctgg tcgcccattta ctttgcata caggttagtat ttgacaagag cgacttggcc 1920  
aaatactcag cgggtggaca ccatcaccat caccattaa 1959

<210> 29  
<211> 507  
<212> PRT  
60 <213> Artificial Sequence

<220>  
 <223> Human P501S (amino acids 55-553) fused to 6 histidine residues

5    <400> 29  
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 Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg  
      20            25            30  
 10   Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu  
      35            40            45  
 Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg  
      50            55            60  
 Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe  
 15   65            70            75            80  
 Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu  
      85            90            95  
 Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe  
      100            105            110  
 20   Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp  
      115            120            125  
 Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys  
      130            135            140  
 Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr  
 25   145            150            155            160  
 Leu Leu Val Ala Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu  
      165            170            175  
 Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala  
      180            185            190  
 30   Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln  
      195            200            205  
 Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu  
      210            215            220  
 Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp  
 35   225            230            235            240  
 Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly  
      245            250            255  
 Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser Leu  
      260            265            270  
 40   Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val Met  
      275            280            285  
 Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala Ser  
      290            295            300  
 Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His Ser  
 45   305            310            315            320  
 Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe Ser  
      325            330            335  
 Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg Glu  
      340            345            350  
 50   Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala Ser  
      355            360            365  
 Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly  
      370            375            380  
 Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu  
 55   385            390            395            400  
 Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser Val  
      405            410            415  
 Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly Arg  
      420            425            430  
 60   Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu Ser  
      435            440            445

Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser Gln  
 450 455 460  
 Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val Ala  
 465 470 475 480  
 5 Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys  
 485 490 495  
 Tyr Ser Ala Gly Gly His His His His His His  
 500 505

10 <210> 30  
 <211> 1524  
 <212> DNA  
 <213> Artificial Sequence

15 <220>  
 <223> DNA encoding Human P501S (amino acids 55-553)  
 fused to 6 histidine residues

20 <400> 30  
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 agtgaccact ggcgtggacg ctatggccgc cgccggccct tcatactggc actgtccttg 120  
 ggcatacctgc tgagccctt tctcatccca agggccggct ggctagcagg gctgtgtgc 180  
 ccggatccca ggccccctgga gctggcaactg ctatcctgg gctgggggt gctggacttc 240  
 25 tgcgtggcagg tgcgtttcac tccactggag gcccgtctt ctgacatctt ccgggaccgg 300  
 gaccactgtc gccaggccta ctctgttat gccttcatga tcagtcttgg gggctgcctg 360  
 ggctacatcc tgcctgcccatt tgactggac accagtgcctt tggcccccata cctgggcacc 420  
 caggaggagt gctcttttgg cctgctcacc ctatcttcc tcacctgcgt agcagccaca 480  
 ctgctggtgg ctgaggaggc agcgctggc cccaccgagc cagcagaagg gctgtcggcc 540  
 30 ccctccttgc tcccccaactg ctgtccatgc cggggccgt tggcttccg gAACCTGGGc 600  
 gccctgcttc cccggctgca ccagctgtc tgccgcattgc cccgcacccct ggcggggctc 660  
 ttctgtggctg agctgtgcag ctggatggc ctatgaccc tcacgtctt ttacacggat 720  
 ttctgtggcg agggggctgta ccaggggctg cccagagctg agccggcacc cggggccgg 780  
 agacactatg atgaaggcgct tgctggggc accgtggggc ttgtctgca gtgcggccatc 840  
 35 tccctggctc tctctctggat catggacccgg ctggtgcagc gattcggcac tcgagcagtc 900  
 tatttggcca gtgtggcage ttccctgtg gctggccgtg ccacatgcgt gtcccacagt 960  
 gtggccgtgg tgacagcttc agccggccctc accgggttca ccttctcagc cctgcagatc 1020  
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 40 cctaagcctg gagctccctt ccctaattggc cactgtgggtg ctggaggcag tggccgtctc 1200  
 ccaccccttcc acggcgctctg cggggccctt gcctgtatg tctccgtacg tgggtgggt 1260  
 ggtgagggcca cggaggccctg ggtgggtccg ggccggggca tctggctgaa cctcgccatc 1320  
 ctggatagtg ctteccctgtgt gtcctggatg gccccatccc ttgttatggg ctccattgtc 1380  
 cagctcagcc agtctgtcac tgcctatatg gtgtctgcgg caggcctggg tctggtcgcc 1440  
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 ggacaccatc accatcacca tttaa 1524

<210> 31  
 <211> 685

50 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human P501S (amino acids 1-34 fused to 55-553)  
 fused to 6 histidine residues

55 <400> 31  
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 60 Lys Ala Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val  
 20 25 30

Cys Leu Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp  
 35 40 45  
 Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly  
 50 55 60  
 5 Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr  
 65 70 75 80  
 Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala  
 85 90 95  
 Asp Lys Trp Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp  
 10 100 105 110  
 Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala  
 115 120 125  
 Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly  
 130 135 140  
 15 Val Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp  
 145 150 155 160  
 Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe  
 165 170 175  
 Met Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val  
 20 180 185 190  
 Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg  
 195 200 205  
 Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu  
 210 215 220  
 25 Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp  
 225 230 235 240  
 Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly Val Gly Leu Leu  
 245 250 255  
 Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser  
 30 260 265 270  
 Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr  
 275 280 285  
 Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala  
 290 295 300  
 35 Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu  
 305 310 315 320  
 Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala  
 325 330 335  
 Ala Thr Leu Leu Val Ala Glu Ala Ala Leu Gly Pro Thr Glu Pro  
 40 340 345 350  
 Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys  
 355 360 365  
 Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu  
 370 375 380  
 45 His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val  
 385 390 395 400  
 Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr  
 405 410 415  
 Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu  
 50 420 425 430  
 Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly  
 435 440 445  
 Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu  
 450 455 460  
 55 Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu  
 465 470 475 480  
 Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser  
 485 490 495  
 His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr  
 60 500 505 510  
 Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His

515	520	525														
Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	
530						535				540						
545							550			555					560	
Pro	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	
565								570			575					
Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	
580								585			590					
10	Ser	Val	Arg	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	
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Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	
610						615				620						
15	Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu
625						630			635			640				
Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	
645							650			655						
20	Val	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu
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25	<210> 32	26	<211> 2058	27	<212> DNA	28	<213> Artificial Sequence	29	<220>	30	<223> DNA encoding Human P501S (amino acids 1-34 fused to 55-553) fused to 6 histidine residues	31	<400> 32	32	atggcggccg	33	tgcagaggct	34	atgggtatcg	35	agactgctaa	36	gacaccgcaa	37	agctcagttg	38	60
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 cccacccgagg ccagggtggg tccggggccgg ggcacatctgcc tggacactgc catcctggat 1860  
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 <212> PRT  
 <213> Artificial Sequence

15 <220>  
 <223> St. pneum. C-LytA portion fused to P2 T helper  
 epitope fused to Human P501S (amino acids 55-553)  
 fused to 6 histidine residues downstream of yeast  
 alphapreproto signal sequence

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 25 Lys Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Phe Asp Ser  
 35 40 45  
 Ser Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn  
 50 55 60  
 Trp Tyr Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys  
 30 65 70 75 80  
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 130 135 140  
 Gly Trp Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu  
 40 145 150 155 160  
 Lys Phe Met Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val  
 165 170 175  
 Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr  
 180 185 190  
 45 Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu  
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 50 225 230 235 240  
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 260 265 270  
 55 Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu  
 275 280 285  
 Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr  
 290 295 300  
 Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys  
 60 305 310 315 320  
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	340	345	350	
5	Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro			
	355	360	365	
	Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu			
	370	375	380	
	Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu			
	385	390	395	400
10	Phe Tyr Thr Asp Phe Val Gly Leu Tyr Gln Gly Val Pro Arg			
	405	410	415	
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	420	425	430	
	Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe			
15	435	440	445	
	Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val			
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	Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys			
	465	470	475	480
20	Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly			
	485	490	495	
	Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu			
	500	505	510	
	Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr			
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	Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly			
	530	535	540	
	Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly			
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30	Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys			
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35	595	600	605	
	Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val			
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	Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu			
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40	Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser			
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	<212> DNA			
	<213> Artificial Sequence			
50	<220>			
	<223> DNA encoding St. pneum. C-LytA portion fused to P2			
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	55-553) fused to 6 histidine residues downstream			
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	aagtggtaact atttcaacga agaagggtcc atgaagacag gctgggtcaa gtacaaggac 240			

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40 <210> 35  
 <211> 595  
 <212> PRT  
 <213> Artificial Sequence

45 <220>  
 <223> Human P501S (amino acids 55-553) fused to 6  
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 signal sequence

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 55 Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe Asp  
 35 40 45  
 Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu Phe  
 50 55 60  
 Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val Ser  
 65 70 75 80  
 Leu Glu Lys Arg Glu Ala Glu Ala Met Val Leu Gly Ile Gly Pro Val

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	Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala		
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	Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile		
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	Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg		
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	Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu		
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	Gly Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro		
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	Tyr Leu Gly Thr Gln Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile		
	225 230 235 240		
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	260 265 270		
	Pro His Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly		
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	Ala Leu Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr		
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	Leu Arg Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met		
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30	Thr Phe Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln		
	325 330 335		
	Gly Val Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp		
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40	Gly Ala Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala		
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	Ala Leu Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr		
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	Leu Ala Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr		
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	450 455 460		
	Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val		
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50	Gly Ala Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly		
	485 490 495		
	Ala Ser Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr		
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	Glu Ala Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile		
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	Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met		
	530 535 540		
	Gly Ser Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser		
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 His His His  
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 10 <213> Artificial Sequence  
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 fused to 6 histidine residues downstream of yeast  
 15 alphaprepro signal sequence  
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 gggagccac acggggctagg gtcgtgcctg gcccggggat ctgcctggac ctggccatcc 1860  
 tcgacteege cttctgtctc tcccaggtgg cggccagctt gttcatgggc agtacgtgc 1920  
 agctgagcca gaggcgtgacc gcttacatgg tgagcgcgcg cggccctgggg ttgggtggca 1980  
 15 tctactttgc caccctggtc gtgtcgaca agagcgatct cgccaaatgtat agcgctgtag 2040  
 gatcc 2045

<210> 39  
 <211> 2105  
 20 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> DNA encoding St.pneum. C-LytA P2 helper epitope  
 25 C-LytA fused to Human P501S (amino acids 51-553)  
 fused to Human P501S (amino acids 1-50) -  
 Codon-optimised

<400> 39

30 gcgcccgcc caccatggcc gcccctacg tgcatacgca cgggagctac cccaaaggaca 60  
 agttcgagaa gatcaacggg acatggact acttcgactc ctccggctac atgctcgccg 120  
 accgctggcg gaagcacacc gacggcaact ggtactgggt cgataactcg ggagagatgg 180  
 ccacccggctg gaagaagatc gcgacaaatg ggtactatcc caacggagg ggcgcctatga 240  
 agacccggctg ggtaaatg aaggacaccc ggtactaccc cgacccaaag gaggccgcca 300  
 35 tgcgtatatac aaggccaaac agcaatgtca tcggcatcac cggggagtg atggtcagca 360  
 acgcctttat ccagagcgc gacggcaccc gatggacta cttgaagccg gacggccccc 420  
 tcgcggatcg gcccggaaag ttcatgtaca tggtgctggg catcgccccc tgcctggcc 480  
 tcgtgtgtgt gcccctccctc gggagtgcgt ccgtatccatg gcgccggccg tacggccgccc 540  
 gcagaccgtt catctggggc ctgagccctgg gcatccctgt ctctctcttc ctgatcccc 600  
 40 gggccggctg gtcgtggggc ctgctgtgtc cggacccccc ccctctggag ctggccctcc 660  
 tgcgtctggg ctgtggccctg ctggacttcc gggcccgatgt gtgttcaact cccctggagg 720  
 ctctgtctc cgaccccttc cggcggccccc accactgttag gcaaggatcc acgtgttacg 780  
 ctttcatgtat cagtgtgggg ggtatgttcc gctatctgt gcccgtatc gactgggaca 840  
 ccagcccccctt gggccctac ctggggactc aggaggagtg cctgttcggc ctgctcacct 900  
 45 tgcgttccat gacgtgcgtc gcccacccc tgcgtggggc cgaggaggccg gcccctggggc 960  
 ccacccggcc gcccggggc ctgagccgtc ccagccgttag ccccccattgc tgcctgtca 1020  
 gggctaggct cgccttcagg aatctggcg cttgtgtcc cgcctgtat cagctgtgt 1080  
 gtcgcattcc tgcacccctg cggccctgt tcgtgcgtga gctctgttcc tggatggccc 1140  
 tgcgtacgtt cacccttcc tacaccgact tcgtggggga ggcctgtac cagggcgtgc 1200  
 50 ccagggccga gcccggcacc gaggctaggc gccattacga cgaggccgtc aggatgggt 1260  
 ctctggggctt ctgcgtgtc tgcgcattca gtcgtgggtt ctctctgggt atggacccgc 1320  
 tggtgacgcg ctggccacc cggccctgt acctcgccctc tggccgggtt ttccccgtcg 1380  
 cccggccggc gacctgcctg ttcattccatc tcgcgtgggt gaccggccacg gcccctgtca 1440  
 cccgcttccatc ttcagtgcg ctccagatcc tgccttacac cctggcgctt ctgtaccatc 1500  
 55 gcgagaagca ggtgttccctg cccaaatgtacc gggggggacac agggggagct tccctgtagg 1560  
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 atgtcgggggc gggccggcacc ggcctgtcc cttccccccccc cggccctgtc ggcgttagt 1680  
 cttcgacgt gaggcgtgggg gttgtgggtgg gggagccccc cggaggctagg gtcgtgcctg 1740  
 gcccggggat ctgcctggac ctggccatcc tcgactccgc ttcctgtc tcccaagggtgg 1800  
 60 cggccagctt gttcatgggc agtacgtgc agtgcgtacca gaggcgtacc gcttacatgg 1860  
 tgagcgcgcg cggccctgggg ttgggtggca ttcactttgc caccctggtc gtgttcgaca 1920

agagcgatct cgccaaagtat agcgccatgg tgcagcggct gtgggtgtcc cggctgctgc 1980  
 gccatagaaa ggcgcagttt ctgctggta acctgctgac tttcggactg gagggtgtcc 2040  
 tggctgccgg gatcacgtac gtgcgggggg tgcgtgtgg ggtgggcgtg gaggagttag 2100  
 gatcc 2105

5 <210> 40  
 <211> 2105  
 <212> DNA  
 <213> Artificial Sequence

10 10 <220>  
 <223> DNA encoding Human P501S (amino acids 1-50) fused  
 to St.pneum. C-LytA P2 helper epitope C-LytA fused  
 to Human P501S (amino acids 51-553) -

15 15 Codon-optimised

<400> 40  
 gcggccgcgc caccatgggt cagcggtgt ggggtgtcccg gctgctgcgc catagaaagg 60  
 cccagttgtct gctggtaaac ctgctgactt tcggactggaa ggtgtgcctg gctgcggga 120  
 20 tcacgtacgt gccccccctgt ctgctggagg tggcggtggaa ggagatggcc gccgcctacg 180  
 tgcatacgca cggggagctac cccaaaggaca agttcgagaa gatcaacggg acatggtaact 240  
 acttcgactc ctccggctac atgcgtccgg accgctggcg gaagcacacc gacggcaact 300  
 ggtactgggtt cgataactcg ggagagatgg ccaccggctg gaagaagatc gcggacaagt 360  
 ggtactattt caacgaggag ggccgcattaa agaccggctg ggtgaagttt aaggacac 420  
 25 ggtactaccc cgacgcacaaag gaggggcgcc tgcgtatcat caaggccaaac agcaagttca 480  
 tcggcatcac cggggggatgttgcgttcc acgcgtttt ccagagccgc gacggcaccc 540  
 gatggactaa cttgaagccg gacggccccc tcgcggatcg gcccggaaat ttcatgtaca 600  
 tgggtctggg catcgcccccc gtcctggcc tcgtgtgtgt gccccctccccc gggagttcggt 660  
 30 ccgatcattt gggggggccgc tacggccccc gcacggcgat ttcgtggcc ctgagccctgg 720  
 gcatctgtct ctctctttt ctgtatcccccc gggccggctg gctggccggc ctgctgtgtc 780  
 ccgacccccc cccctctggag ctggccctcc tgatcctggg cgtggccctg ctggacttct 840  
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 35 gctatctgtct gccccctatac gactggggaca ccacgccttcc gggcccttac ctggggactc 1020  
 aggaggagtgc cttgttcggc ctgttccactt tgatcttccat gacgtgcgtc gccgcacccc 1080  
 tgctgggtggc cgaggaggcg gcccctgggc ccacccggacc cggccggggc ctgagccgtc 1140  
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 ctttctgtcc cccctctgtcat cagctgtgtc gtgcgtatgcc tgcaccccttgc cggccctgt 1260  
 tcgtcgctgtatgtctgtcc tggatggccc tgatgacgtt cacccttc tacaccgact 1320  
 40 tcgtggggggat gggctgtac cagggcggtc ccacggccgc gcccggcacc gaggctaggc 1380  
 gccattacgtcgaggccgtc aggatgggtt ctctggcccttccctgcagtg tgcgcacatca 1440  
 gtctgggtttt ctctctgtgtt atggacccggc tgggtcgacgc cttccgcacc cggccgtgt 1500  
 acctcgccctc tggggggggatcccttcgtcc cccggccgc gacctgccttgc ttcattctg 1560  
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 45 tgcctctacac cctggcgctt ctgtaccatc gcgagaagac ggtgttccctg cccaaatgtacc 1680  
 ggggggacac agggggggatcccttcgttccatc gacggctgtat gaccagccctt tggccggcc 1740  
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 50 tcgactccgc tttccatgttcc tcccaggatgtt cggccgttccat gttcatggc agtatacggtc 1980  
 agtgagcca gagggtgtacc gcttacatgg tgagcgccgc cggccctgggg tttggggcca 2040  
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 gatcc 2105

55 55 <210> 41  
 <211> 652  
 <212> PRT  
 <213> Artificial Sequence

60 60 <220>  
 <223> St.pneum. C-LytA P2 helper epitope C-LytA fused to

## Human P501S

<400> 41  
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 5 1 5 10 15  
 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Phe Asp Ser Ser Gly Tyr  
 20 25 30  
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp  
 35 40 45  
 10 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp  
 50 55 60  
 Lys Trp Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val  
 65 70 75 80  
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met  
 15 85 90 95  
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val  
 100 105 110  
 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr  
 115 120 125  
 20 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met  
 130 135 140  
 Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro  
 145 150 155 160  
 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg  
 25 165 170 175  
 Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe  
 180 185 190  
 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro  
 195 200 205  
 30 Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp  
 210 215 220  
 Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp  
 225 230 235 240  
 Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala  
 35 245 250 255  
 Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile  
 260 265 270  
 Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu  
 275 280 285  
 40 Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala  
 290 295 300  
 Thr Leu Leu Val Ala Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala  
 305 310 315 320  
 Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg  
 45 325 330 335  
 Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His  
 340 345 350  
 Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala  
 355 360 365  
 50 Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr  
 370 375 380  
 Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro  
 385 390 395 400  
 Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser  
 55 405 410 415  
 Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val  
 420 425 430  
 Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala  
 435 440 445  
 60 Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His  
 450 455 460

Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe  
 465 470 475 480  
 Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg  
 485 490 495  
 5 Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala  
 500 505 510  
 Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro  
 515 520 525  
 Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Ser Gly Leu  
 10 530 535 540  
 Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser  
 545 550 555 560  
 Val Arg Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly  
 565 570 575  
 15 Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu  
 580 585 590  
 Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser  
 595 600 605  
 Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val  
 20 610 615 620  
 Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala  
 625 630 635 640  
 Lys Tyr Ser Ala Gly Gly His His His His His His  
 645 650

25

<210> 42  
 <211> 1959  
 <212> DNA  
 30 <213> Artificial Sequence

<220>  
 <223> DNA encoding St.pneum. C-LytA P2 helper epitope  
 C-LytA fused to Human P501S (plus his tag)

35

<400> 42  
 atggcgcccg cttacgtaca ttccgacggc tcttatccaa aagacaagtt tgagaaaatc 60  
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 cacacagacg gcaactggta ctgggtcgac aactcaggcg aaatggctac aggctggaaag 180  
 40 aaaaatcgctg ataagtggta ctatccaaac gaagaagggtg ccatgaagac aggctgggtc 240  
 aagtacaagg acacttggta ctacttagac gctaaagaag gcgccatgca atacatcaag 300  
 gctaactcta agttcattgg tatcaactgaa ggcgtcatgg tatcaaatgc ctttatccag 360  
 tcagcggacg gaacaggctg gtactacctc aaaccagacg gaacactggc agacaggcca 420  
 gaaaagttca tgtacatggt gctgggcatt ggtccagtgc tgggcctgtt ctgtgtcccg 480  
 45 ctcctaggct cagccagtga ccactggcgt ggacgctatg gcccggccg gcccctcatac 540  
 tgggcactgt ctttggccat cctgctgagc ctctttctca tcccaagggc cggctggcta 600  
 gcaggggctgc tggccggc tcccaggccc ctggagctgg cactgctcat cctgggcgtg 660  
 gggctgctgg acttctgtgg ccagggtgtc ttcaactccac tggggccct gctctctgac 720  
 50 ctcttccggg acccgggacca ctgtccggcgc gcctactctg tctatgcctt catgatcagt 780  
 cttgggggtt gcttggctca cttcttgcct ccattgtact gggacaccag tggccctggcc 840  
 ccctacctgg gcaaccaggaa ggagtgcctc tttggctgc tcaccctcat cttccctcacc 900  
 tgcgtacgac ccacactgtt ggtggctgag gaggcagcgc tggggccctac cgagccagca 960  
 gaagggtgtt cggcccccctc cttgtccccc cactgtgtc catgcccggc cccgttggct 1020  
 ttccggaaacc tggggccctt gttcccccgg ctgcaccaggc tggctgtccg catgccccgc 1080  
 55 accctgcgcc ggcttcttgcgt ggctgagctg tgcaagctgaa tggcactcat gacccctac 1140  
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 ggcacccggagg cccggagacaa ctatgtgaa ggcgttccgaa tggggcagcct ggggtgttc 1260  
 ctgcgtgcg ccatctccctt ggtcttctctt ctgtccatgg accggctgtt gcagcgttcc 1320  
 60 ggcactcggc cagtttattt gggcagggtg gcaagtttcc ctgtggctgc cgggtccaca 1380  
 tgctgtccc acagtgtggc cgtggtgaca gcttcagccg ccctcaccgg gttcaccttc 1440  
 tcagccctgc agatcctgcc ctacacactg gcctccctct accaccggga gaagcagggtg 1500

ttcctgccc aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc 1560  
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 5 gtacgtgtgg tgggtgggtga gcccacccgag gccagggtgg ttccggggccg gggcatctgc 1740  
 ctggacctcg ccatccctgga tagtgccttc ctgtgtccc aggtggcccc atccctgttt 1800  
 atgggtccca ttgtccagct cagccagtct gtactgcct atatgggtgc tgccgcaggc 1860  
 ctgggtctgg tcgccattta ctttgctaca caggtagtat ttgacaagag cgacttggcc 1920  
 aaatactcag cgggtggaca ccatcaccat caccattaa 1959

10 <210> 43  
 <211> 553  
 <212> PRT  
 <213> Homo sapiens

15 <400> 43  
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 1 5 10 15  
 Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
 20 25 30  
 20 Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
 35 40 45  
 Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
 50 55 60  
 Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
 25 65 70 75 80  
 Arg Tyr Gly Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
 85 90 95  
 Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
 100 105 110  
 30 Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly  
 115 120 125  
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
 130 135 140  
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
 35 145 150 155 160  
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
 165 170 175  
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
 180 185 190  
 40 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
 195 200 205  
 Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
 210 215 220  
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
 45 225 230 235 240  
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
 245 250 255  
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
 260 265 270  
 50 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
 275 280 285  
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
 290 295 300  
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 55 305 310 315 320  
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
 325 330 335  
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
 340 345 350  
 60 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
 355 360 365

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
 370 375 380  
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
 385 390 395 400  
 5 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
 405 410 415  
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
 420 425 430  
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
 10 435 440 445  
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser  
 450 455 460  
 Ala Cys Asp Val Ser Val Arg Val Val Gly Glu Pro Thr Glu Ala  
 465 470 475 480  
 15 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
 485 490 495  
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
 500 505 510  
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
 20 515 520 525  
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
 530 535 540  
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
 545 550

25

<210> 44  
 <211> 644  
 <212> PRT  
 30 <213> Artificial Sequence

<220>  
 <223> St.pneum. C-LytA P2 helper epitope C-LytA fused to  
 Human P501S

35

<400> 44  
 Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys  
 1 5 10 15  
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 40 20 25 30  
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp  
 35 40 45  
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp  
 50 55 60  
 45 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val  
 65 70 75 80  
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met  
 85 90 95  
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val  
 50 100 105 110  
 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr  
 115 120 125  
 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met  
 130 135 140  
 55 Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro  
 145 150 155 160  
 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg  
 165 170 175  
 Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe  
 60 180 185 190  
 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro

	195	200	205	
	Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp			
	210	215	220	
	Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp			
5	225	230	235	240
	Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala			
	245	250	255	
	Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile			
	260	265	270	
10	Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu			
	275	280	285	
	Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala			
	290	295	300	
	Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala			
15	305	310	315	320
	Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg			
	325	330	335	
	Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His			
	340	345	350	
20	Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala			
	355	360	365	
	Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr			
	370	375	380	
	Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro			
25	385	390	395	400
	Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser			
	405	410	415	
	Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val			
	420	425	430	
30	Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala			
	435	440	445	
	Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His			
	450	455	460	
	Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe			
35	465	470	475	480
	Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg			
	485	490	495	
	Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala			
	500	505	510	
40	Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro			
	515	520	525	
	Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu			
	530	535	540	
	Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser			
45	545	550	555	560
	Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly			
	565	570	575	
	Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu			
	580	585	590	
50	Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser			
	595	600	605	
	Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val			
	610	615	620	
	Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala			
55	625	630	635	640
	Lys Tyr Ser Ala			
60	<210> 45			
	<211> 644			

<212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

5 <223> Codon-optimised hybrid protein between St.pneum. C-LytA P2  
 helper epitope C-LytA fused to Human P501S  
 amino acids 51-553)

10 <400> 45  
 Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys  
 1 5 10 15  
 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr  
 20 25 30  
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp  
 15 35 40 45  
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp  
 50 55 60  
 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val  
 65 70 75 80  
 20 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met  
 85 90 95  
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val  
 100 105 110  
 25 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr  
 115 120 125  
 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met  
 130 135 140  
 Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro  
 145 150 155 160  
 30 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg  
 165 170 175  
 Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe  
 180 185 190  
 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro  
 35 195 200 205  
 Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp  
 210 215 220  
 Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp  
 225 230 235 240  
 40 Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala  
 245 250 255  
 Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile  
 260 265 270  
 Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu  
 45 275 280 285  
 Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala  
 290 295 300  
 Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala  
 305 310 315 320  
 50 Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg  
 325 330 335  
 Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His  
 340 345 350  
 Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala  
 55 355 360 365  
 Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr  
 370 375 380  
 Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro  
 385 390 395 400  
 60 Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser  
 405 410 415

Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val  
 420 425 430  
 Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala  
 435 440 445  
 5 Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His  
 450 455 460  
 Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe  
 465 470 475 480  
 Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg  
 10 485 490 495  
 Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala  
 500 505 510  
 Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro  
 515 520 525  
 15 Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Ser Gly Leu  
 530 535 540  
 Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser  
 545 550 555 560  
 Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly  
 20 565 570 575  
 Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu  
 580 585 590  
 Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser  
 595 600 605  
 25 Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val  
 610 615 620  
 Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala  
 625 630 635 640  
 Lys Tyr Ser Ala  
 30

<210> 46  
 <211> 694  
 35 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> St.pneum. C-LytA P2 helper epitope C-LytA fused to  
 40 Human P501S (amino acids 1-553) - codon optimised

<400> 46  
 Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys  
 1 5 10 15  
 45 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr  
 20 25 30  
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp  
 35 40 45  
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp  
 50 55 60  
 50 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val  
 65 70 75 80  
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met  
 85 90 95  
 55 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val  
 100 105 110  
 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr  
 115 120 125  
 60 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Met Val Gln  
 130 135 140  
 Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala Gln Leu Leu

145	150	155	160
Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu Ala Ala Gly			
165	170	175	
Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys			
180	185	190	
Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys			
195	200	205	
Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly			
210	215	220	
10 Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser			
225	230	235	240
Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro			
245	250	255	
Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu			
15 260	265	270	
Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu			
275	280	285	
Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val			
290	295	300	
20 Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro			
305	310	315	320
Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln			
325	330	335	
Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val			
25 340	345	350	
Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu			
355	360	365	
Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro			
370	375	380	
30 Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg			
385	390	395	400
Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe			
405	410	415	
Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe			
420	425	430	
35 Tyr Thr Asp Phe Val Gly Glu Leu Tyr Gln Gly Val Pro Arg Ala			
435	440	445	
Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met			
450	455	460	
40 Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser			
465	470	475	480
Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr			
485	490	495	
Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu			
45 500	505	510	
Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe			
515	520	525	
Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr			
530	535	540	
50 His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly			
545	550	555	560
Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro			
565	570	575	
Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser			
55 580	585	590	
Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp			
595	600	605	
Val Ser Val Arg Val Val Gly Glu Pro Thr Glu Ala Arg Val Val			
610	615	620	
60 Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe			
625	630	635	640

Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln  
 645 650 655  
 Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly  
 660 665 670  
 5 Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp  
 675 680 685  
 Leu Ala Lys Tyr Ser Ala  
 690

10 <210> 47  
 <211> 694  
 <212> PRT  
 <213> Artificial Sequence

15 <220>  
 <223> St.pneum. C-LytA P2 helper epitope C-LytA fused to  
 Human P501S (amino acids 51-553) fused to Human  
 P501S (amino acids 1-50) - codon-optimised

20 <400> 47  
 Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys  
 1 5 10 15  
 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Phe Asp Ser Ser Gly Tyr  
 20 25 30  
 25 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp  
 35 40 45  
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp  
 50 55 60  
 30 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val  
 65 70 75 80  
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met  
 85 90 95  
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val  
 100 105 110  
 35 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr  
 115 120 125  
 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met  
 130 135 140  
 40 Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro  
 145 150 155 160  
 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg  
 165 170 175  
 Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe  
 180 185 190  
 45 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro  
 195 200 205  
 Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp  
 210 215 220  
 50 Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp  
 225 230 235 240  
 Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala  
 245 250 255  
 Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile  
 260 265 270  
 55 Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu  
 275 280 285  
 Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala  
 290 295 300  
 60 Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala  
 305 310 315 320

Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg  
 325 330 335  
 Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His  
 340 345 350  
 5 Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala  
 355 360 365  
 Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr  
 370 375 380  
 Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro  
 10 385 390 395 400  
 Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser  
 405 410 415  
 Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val  
 420 425 430  
 15 Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala  
 435 440 445  
 Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His  
 450 455 460  
 Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe  
 20 465 470 475 480  
 Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg  
 485 490 495  
 Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala  
 500 505 510  
 25 Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro  
 515 520 525  
 Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu  
 530 535 540  
 Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser  
 30 545 550 555 560  
 Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly  
 565 570 575  
 Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu  
 580 585 590  
 35 Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser  
 595 600 605  
 Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val  
 610 615 620  
 Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala  
 40 625 630 635 640  
 Lys Tyr Ser Ala Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg  
 645 650 655  
 His Arg Lys Ala Gln Leu Leu Val Asn Leu Leu Thr Phe Gly Leu  
 660 665 670  
 45 Glu Val Cys Leu Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu  
 675 680 685  
 Glu Val Gly Val Glu Glu  
 690

50 <210> 48  
 <211> 694  
 <212> PRT  
 <213> Artificial Sequence

55 <220>  
 <223> Human P501S (amino acids 1-50) fused to St.pneum.  
 C-LytA P2 helper epitope C-LytA fused to Human  
 P501S (amino acids 51-553) - codon optimised

60 <400> 48

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala  
 1 5 10 15  
 Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
 20 25 30  
 5 Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
 35 40 45  
 Glu Glu Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys  
 50 55 60  
 10 Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser  
 65 70 75 80  
 Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp  
 85 90 95  
 Tyr Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile  
 100 105 110  
 15 Ala Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly  
 115 120 125  
 Trp Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly  
 130 135 140  
 20 Ala Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu  
 145 150 155 160  
 Gly Val Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly  
 165 170 175  
 Trp Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys  
 180 185 190  
 25 Phe Met Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys  
 195 200 205  
 Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly  
 210 215 220  
 30 Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser  
 225 230 235 240  
 Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro  
 245 250 255  
 Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly Val Gly Leu  
 260 265 270  
 35 Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu  
 275 280 285  
 Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val  
 290 295 300  
 Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro  
 40 305 310 315 320  
 Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln  
 325 330 335  
 Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val  
 340 345 350  
 45 Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu  
 355 360 365  
 Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro  
 370 375 380  
 Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg  
 50 385 390 395 400  
 Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe  
 405 410 415  
 Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe  
 420 425 430  
 55 Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala  
 435 440 445  
 Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met  
 450 455 460  
 60 Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser  
 465 470 475 480  
 Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr

	485	490	495
	Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu		
	500	505	510
5	Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe		
	515	520	525
	Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr		
	530	535	540
	His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly		
	545	550	555
10	Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro		
	565	570	575
	Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser		
	580	585	590
	Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp		
15	595	600	605
	Val Ser Val Arg Val Val Gly Glu Pro Thr Glu Ala Arg Val Val		
	610	615	620
	Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe		
	625	630	635
20	Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln		
	645	650	655
	Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly		
	660	665	670
	Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp		
25	675	680	685
	Leu Ala Lys Tyr Ser Ala		
	690		
30	<210> 49		
	<211> 1971		
	<212> DNA		
	<213> Artificial Sequence		
35	<220>		
	<223> DNA encoding Human MUC-1 fused to St.pneum. C-LytA		
	P2 helper epitope C-LytA		
	<400> 49		
40	atgacacccgg gcacccagtc tcctttcttc ctgctgctgc tcctcacagt gcttacagtt 60		
	gttacagggtt ctggcatgc aagctctacc ccaggtggag aaaaggagac ttccggctacc 120		
	cagagaaggtt cagtggccag ctctactgag aagaatgctg tgagttatgac cagcagcgta 180		
	ctctccagcc acagccccggg ttcaggttcc tccaccactc agggacagga tgcactctg 240		
	gccccggcca cggaaaccagc ttcaggttca gtcggccacctt ggggacagga tgcacccctcg 300		
45	gtcccagtca ccaggccagc cctgggttcc accacccccgc cagcccacaga tgcacccctcg 360		
	gccccggaca acaaggccagc cccgggttcc accggggggcc cagcccacgg tgcacccctcg 420		
	gccccggaca ccaggccggcc cccgggttcc accggggggcc cagcccacgg tgcacccctcg 480		
	gccccggaca ccaggccggcc cccgggttcc accggggggcc cagcccacgg tgcacccctcg 540		
50	gccccggaca ccaggccggcc cccgggttcc accggggggcc cagcccacgg tgcacccctcg 600		
	gccccggaca acaggccggcc cttgggttcc accggggggcc cagttccacaaa tgcacccctcg 660		
	gcctcagggtt ctgcattcagg ctcaatctt actctgggttgc acaacggcac ctctggcagg 720		
	gttaccacaa ccccaagccag caagggactt ccattctcaa ttcccgccca ccactctgtat 780		
	actcttacca cccttgcacccatgc ccatagccacc aagactgtat ccagtagccac tcaccatgc 840		
	acggtaatctc ctctcaccatcc ctccaaatccatgc agcaatctc cccagttgttca tactgggttca 900		
55	tctttttttt tcctgttctt tcacattca aacctccagt ttaattccctc tctggaaat 960		
	cccaacccgg actactacca agagctgcag agagacattt ctgaaatgtt tttgcagatt 1020		
	tataaaacaag ggggttttttcttcc aatattaatgt tcaggccagg atctgtgggtt 1080		
	gtacaattgtt ctctggccctt ccggagaatgtt accatcaatgt tccacgcacgtt ggagacacag 1140		
60	ttcaatctgtt ataaaacccggaa agcagcttccatgc cgtatataacc tgacgttcc agacgtcagg 1200		
	gtgatgttgc tgccatttcc tttctctgttcc cagtttttttttccatgttcc tctcatttgc 1260		
	atcgctgc tggtgttcttcc ctgtgttcttcc gttgtgttcttccatgttcc tctcatttgc 1320		

ttggctgtct gtcagtgcgg ccgaaagaac tacgggcagc tggacatctt tccagccgg 1380  
 gatacctacc atcctatgag cgagtacccc acctaccaca cccatggcg ctatgtgccc 1440  
 cctagcagta ccgatcgtag cccctatgag aaggttctg caggtaatgg tggcagcagc 1500  
 ctctcttaca caaaccaggc agtggcagcc acttctgcca acttcatggc gggcgcttac 1560  
 5 gtacattccg acggcttta tccaaaagac aagtttggaa aatcaatgg cacttggtag 1620  
 tactttgaca gttcaggctta tatgttgcg gaccgtggaa ggaaggcacac agacggcaac 1680  
 tggtaactggt tcgacaactc agggcaatg gctacaggct ggaagaaaat cgctgataag 1740  
 tggtaactt tcaacgaaga aggtgccatg aagacaggct gggtaagta caaggacact 1800  
 tggtaactact tagacgctaa agaaggcgcc atgcaataca tcaaggctaa ctctaagttc 1860  
 10 attggtatca ctgaaggcgt catggtatca aatgcctta tccagtcagc ggacggaaaca 1920  
 ggctggtaacttcaaaacc agacggaaaca ctggcagaca ggccagaatg a 1971

<210> 50  
 <211> 656  
 15 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human MUC-1 fused to St.pneum. C-LytA P2 helper  
 20 epitope C-LytA

<400> 50  
 Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr  
 1 5 10 15  
 25 Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly  
 20 25 30  
 Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser  
 35 40 45  
 Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His  
 50 55 60  
 30 Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu  
 65 70 75 80  
 Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln  
 85 90 95  
 35 Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr  
 100 105 110  
 Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro  
 115 120 125  
 40 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr  
 130 135 140  
 Arg Pro Pro Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser  
 145 150 155 160  
 Ala Pro Asp Thr Arg Pro Pro Gly Ser Thr Ala Pro Ala Ala His  
 165 170 175  
 45 Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala  
 180 185 190  
 Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu  
 195 200 205  
 50 Ala Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser  
 210 215 220  
 Ala Ser Gly Ser Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg  
 225 230 235 240  
 Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser  
 245 250 255  
 55 His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr  
 260 265 270  
 Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser  
 275 280 285  
 60 Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe  
 290 295 300  
 Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp

305	310	315	320
	Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met		
	325	330	335
5	Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile		
	340	345	350
	Lys Phe Arg Pro Gly Ser Val Val Gln Leu Thr Leu Ala Phe Arg		
	355	360	365
	Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr		
	370	375	380
10	Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser		
	385	390	395
	Val Ser Asp Val Pro Phe Pro Ser Ala Gln Ser Gly Ala Gly Val		
	405	410	415
	Pro Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala		
15	420	425	430
	Leu Ala Ile Val Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg		
	435	440	445
	Lys Asn Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His		
	450	455	460
20	Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro		
	465	470	475
	Pro Ser Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn		
	485	490	495
	Gly Gly Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Thr Ser		
25	500	505	510
	Ala Asn Leu Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro		
	515	520	525
	Lys Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser		
	530	535	540
30	Ser Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn		
	545	550	555
	Trp Tyr Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys		
	565	570	575
	Ile Ala Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr		
35	580	585	590
	Gly Trp Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu		
	595	600	605
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665

670

5